IN THE SPECIFICATION:

Please replace the existing title with the following title:

--ION-157 ION CHANNEL POLYPEPTIDE--

Please amend paragraph **[000265]** as follows:

-- A brief description of the searching mechanism follows. The BLAST algorithm, Basic Local Alignment Search Tool, is suitable for determining sequence similarity (Altschul *et al.*, *J. Mol. Biol.*, 1990, *215*, 403-410, which is incorporated herein by reference in its entirety). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (webpage with the worldwide web (www) address ~~www.~~cbi.nlm.nih.gov/). This algorithm involves first identifying high scoring sequence pair (HSPs) by identifying short words of length "W" in the query sequence that either match or satisfy some positive valued threshold score "T" when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al., supra*). These initial neighborhood word hits act as seeds for initiating searches to find HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Extension for the word hits in each direction are halted when: 1) the cumulative alignment score falls off by the quantity X from its maximum achieved value; 2) the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or 3) the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment. The BLAST program uses as defaults a word length (W) of 11, the BLOSUM62 scoring matrix (*see* Henikoff *et al.*, *Proc. Natl. Acad. Sci. USA*, 1992, *89*,10915-19, which is incorporated herein by reference in its entirety) alignments (B) of 50, expectation (E) of 10, M=5, N=4, and a comparison of both strands. --

Please amend paragraph **[000312]** as follows:

-- PCR was carried out using 3 Units/100 µl of Amplitaq Gold DNA Polymerase (Perkin-Elmer), 1.5 mM $MgCl_2$, 0.2mM dNTPs mix, 0.5 µM of each primer, and 50 ng of Stanford G3 Radiation Hybrid Panel genomic DNA per 25 µl reaction. The Stanford G3 Radiation Hybrid Panel was purchased from Research Genetics, Inc. and was used to perform medium resolution radiation hybrid mapping (RHM). RHM is a PCR based method for determining the cytogenetic location of a unique sequence in the human genome. Each primer set was used to PCR the complete panel twice, on separate days, unless another "Ion" novel sequence had been grouped with it (due to sequence overlap), or had already been subject to RHM and generated the same profile. Data profiles consisting of the presence or absence of the appropriate size PCR product across the panel of 83 radiation hybrid clones were submitted to the Stanford Radiation Hybrid Mapping server at the web site with the worldwide web (www) address shgc.stanford.edu/RH/rhserverformnew.html ~~"www-shgc.stanford.edu/RH/rhserverformnew.html"~~. The data were subjected to two-point statistical analysis with all assayed G3 or TNG radiation hybrid panel markers to determine which markers were most closely linked to the PCR amplified region. The server automatically and anonymously sent back the nearest markers and their associated LOD scores.--

Please amend paragraph **[000313]** as follows

--Ion159 returned markers SHGC-32730 with a LOD score of 17.68, SHGC-2795 with a LOD score of 17.68, SHGC-2792 with a LOD score of 16.95, SHGC-2781 with a LOD score of 16.95 and SHGC-33922 with a LOD score of 15.12, with all located on chromosome 20. The Stanford RHM server was used to obtain further marker location information as well as the GeneMap pages at the National Center for Biotechnology Information (NCBI) site at the worldwide web (www) page: ncbi.nlm.nih.gov/genemap/page.cgi?F=Home.html" ~~"www.ncbi.nlm.nih.gov/genemap/page.cgi?F=Home.html"~~. Ion159 was localized to chromosomal region 20q12-q13.13.--